Panza in gut endoderm suggests that α2M function may be important for differentiation and morphogenesis of the gut. To examine the role of Edd and Panza in gut development, loss-of-function experiments using morpholino oligos (MO) were performed to knockdown Edd and Panza individually and together. Panza knockdown resulted in a ventral bending of the posterior axis, lack of gut coiling, kinking of the notochord and somites defects. Edd knockdown resulted in a shortened body axis, a failure of tail outgrowth, lack of gut coiling, notochord shortening and somites defects. Knockdown of Edd and Panza resulted in shortened body axis, an absence of tail structures, head and eyes defects, lack of gut coiling, notochord degeneration and disorganized somites. Mesodermal and endodermal patterning was examined from the gastrula stage through the coiled gut stage in single and double knockdown embryos. Formation and patterning of the mesoderm and endoderm during gastrula stage and gut morphogenesis was unaffected by Edd or Panza knockdown. These results suggest that α2M function is essential for axial and gut morphogenesis.

doi:10.1016/j.ydbio.2008.05.461

Program/Abstract # 481
Understanding the function of nonmuscle myosin II-A (NM II-A) in vivo
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In vertebrates 3 genes, *Myh*9, *Myh*10 and *Myh*14 encode 3 different isoforms of nonmuscle myosin II heavy chain (NMHC). The motor activity of NM II resides in the N-terminal globular head domain and filament formation resides in the C-terminal rod domain. Previous work has shown that ablation of NM II-A in mice results in lethality by E6.5 with defects in cell–cell adhesion and failure to produce a competent visceral endoderm. To understand the function of NM II-A during development we used homologous recombination to generate 4 different mouse lines: 1—we replaced NM II-A with NM II-B by "knocking in" cDNA encoding NMHC II-B to the II-A locus, thereby ablating II-A and placing NMHC II-B under control of the II-A promoter (A^{b*}/A^{b*} mice). 2—we replaced endogenous NM II-A by knocking in two chimeric NMHCs, one encoding the N-terminal domain of NMHC II-A fused to the C-terminal II-B domain (A^{ab}/A^{ab} mice) and 3—one encoding the N-terminal domain of NMHC II-B fused to the C-terminal II-A domain (A^{ba}/A^{ba} mice). Replacing NM II-A with II-B (A^{b*}/A^{b*}) allows normal development of the visceral endoderm, gastrulation, organogenesis and survival to E9–10. These mice develop a beating heart with defects in vasculature and endocardium. A^{ba}/A^{ba} mice die at a similar age as A^{b*}/A^{b*} mice indicating that the N-terminal domains are interchangeable between II-A and II-B during early development despite differences in kinetic properties of the motors. A^{ab}/A^{ab} mice survive beyond E14 with a hypoplastic heart and an aorta overriding a VSD suggesting that the motor domain of II-A prevents lethality at E9–10. 4-control mice with cDNA encoding NMHC II-A inserted in the II-A locus were normal.

doi:10.1016/j.ydbio.2008.05.462

Program/Abstract # 482
Coordinate regulation of organ morphogenesis in *C. elegans*
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We have previously described a role for the lin-35/Rb tumor suppressor in the organogenesis of the *Caenorhabditis elegans* pharynx. More specifically, our analysis indicates that LIN-35, in conjunction with UBC-18–ARI-1, an E2/E3 complex, redundantly regulates an early step of pharyngeal morphogenesis involved in the orientation of primordial anterior cells of the foregut. Further work has also implicated a novel protein, PHA-1, in this process. Functional redundancy of these pathways is indicted by the observation that lin-35; ubc-18 double mutants, as well as certain allelic combinations of lin-35 and pha-1, display defects in pharyngeal development, whereas single mutants do not. Previous work by Schnabel and colleagues had identified three loci, sup-35, sup-36, and sup-37, which act as strong recessive genetic suppressors of pha-1 single-mutant lethality. All three suppressors also revert the synthetic lethality of lin-35; ubc-18, lin-35; pha-1, and ubc-18; pha-1 double mutants. To gain a better understanding of the networks regulating pharyngeal development, we have cloned sup-35 and sup-37. Both genes encode C2H2 Zn finger proteins, suggesting roles in transcriptional regulation. Using a combination of genetic and molecular analysis, we have obtained evidence suggesting that LIN-35 and UBC-18–ARI-1 function redundantly to negatively regulate SUP-35, which in turn acts as a negative regulator of PHA-1. Our studies have also identified loss-of-function mutations in a phylogenetically conserved protein that may suppress double-mutant lethality through regulation of the LIN-35 binding partner, EFL-1/E2F.

doi:10.1016/j.ydbio.2008.05.463

Program/Abstract # 483
A genetic screen to identify genes necessary for *C. elegans* pharynx muscle development
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The *Caenorhabditis elegans* pharynx provides a simple model to understand the genetics cell patterning and morphogenesis. The pharynx is derived from two blastomeres, the ABa cell, which produces primarily anterior pharynx, and the MS cell, whose decedents are located primarily in the posterior of the organ. Many genes have been shown to be required for development of the anterior pharynx; this may be because pharynx is not the primary cell fate of ABa decedents. In contrast, the MS blastomere is competent to produce the same types of pharynx cells as the ABa, but apparently by a different pathway. We have completed a genetic screen for worms with abnormal pharynx muscle morphology facilitated by an integrated myo-2::GFP reporter gene. We screened 10,000 haploid genomes and have identified close to 200 mutant lines with phenotypically abnormal pharynx. Currently, we are performing snip–SNP mapping and complementation tests to identify the loci of the lesions resulting in the individual phenotypes. We have organized these phenotypes into various groups including blunt/shortened pharynx that may or may not be associated with a Dpy phenotype; pharynx unattached phenotypes, ABa derived cells missing, pharynx muscle outside of the pharynx, diminished anterior bulb, and asymmetric/bulging pharynx. Most of the pharynx phenotypes affect the anterior pharynx, or ABa-derived pharynx muscle cells. We are investigating a few mutants that appear to have reduced posterior pharynx muscle cell size; however, we found no lines with absent posterior myo-2::GFP expression.

doi:10.1016/j.ydbio.2008.05.464